

PCR-based Sanger sequencing of the candidate structural variation breakpoints

The primer sequences of 20 candidate structural variation breakpoints for sanger sequencing

Test ID	Structural variation	Type	Forward primer	Reverse primer
DEL1	11:50549307-50566438	Deletion	TGGTTCTTCTTCTAAGAGAG	AAACTAACCTGGGTACATC
DEL2	1:213629093-213634890	Deletion	GTGGCCTCAAACATATG	CATGCTTAAGAGGGAGTC
DEL3	11:92308840-92310743	Deletion	GCAATATACAGCAAACTAACAG	AGACAGAAAGCTGTTAGGTAG
DEL4	1:262721190-262727474	Deletion	GAGTCGTGATAAACCAAGG	AATTCTTGCGCTGAACC
DEL5	12:38993403-38993665	Deletion	AACCACTGAGCCATCTCTC	CAAGAGGTCATCAGTGGTG
DEL6	1:38086269-38086923	Deletion	AATACTACTGCTCCTGTTCC	ATAGCACACAGTGAATGAAAG
DEL7	1:260655415-260661346	Deletion	AATTGTTTCTGGCACTTC	GAAGAGACTTGAACTTGG
DEL8	1:234160312-234174014	Deletion	CTCTGAGCCTCCAGATAAG	TCAAACCAACCAAAGAGG
DEL9	1:10290542-10305607	Deletion	GTGGTGGCGTTATCAGTAG	GTAAATCCTTCTTCTCCCTG
DEL10	1:13169295-13175227	Deletion	TGATGCCAACTAGCAAGG	TGACCCCTCAGTTACTTCTTC
INV1	5:109309875-109314292	Inversion	GAGAAGAAATAGCTAAGAAATCC	GACTTGATGGAGACTCTAAGAG
INV2	10:101908959-101909081	Inversion	CCCTCCTCCTTCTCTTACTC	GGGAGTCTTAGGCCACTTC
INV3	7:54516805-54530515	Inversion	TTCACCCCTGTGAGGAGAG	AAACGAATGTAACGTGTGG
INV4	1:203464083-203464848	Inversion	AGTCAGACCATCCATTCAC	ATATACACCATCGACTCAGTAG
INV5	5:119914323-119916110	Inversion	ATACCATAACAACCAGATACAAG	ATTCTATTCACTGCAGAG
INV6	11:13008785-13009036	Inversion	AAGAGGCTTACTTGGTTTC	GCCTAATGAAGTATTAGCTG
INV7	5:151993298-151993968	Inversion	AGGCATTTGATGAACAGC	GTCCCTGCATGAGAAGTC
INV8	10:15371453-15372019	Inversion	AATAGTTGACCTTACCATGAC	AGATACATGCAGTATTCAGC
INV9	2:123020464-123022896	Inversion	GCCATTAGACACTGGAGAG	GAGGTGGTATGAGTAATACAAC
INV10	5:115063607-115064257	Inversion	AGTTGGATGACATCAGCC	TTCTGTCTGGCTTGTATACC

Twenty randomly selected deletion and inversion breakpoints were analyzed using polymerase chain reaction (PCR)-based Sanger sequencing with the primers designed according to the de novo assembled scaffolds. For both forward and reverse primer, the sequence was given in 5' to 3' direction.

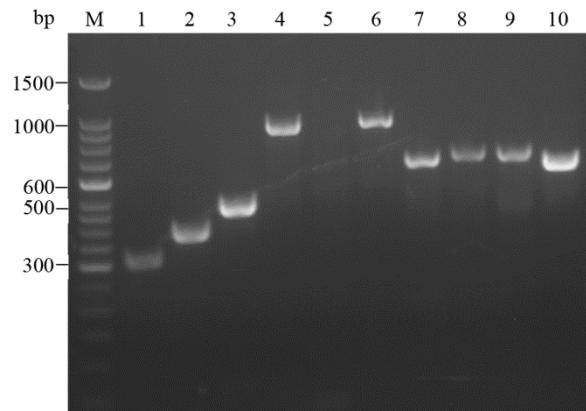


Figure A: PCR results of candidate deletion breakpoints. Lane M: Marker; Lane1–10 represent deletion breakpoints of DEL1–DEL10, respectively.

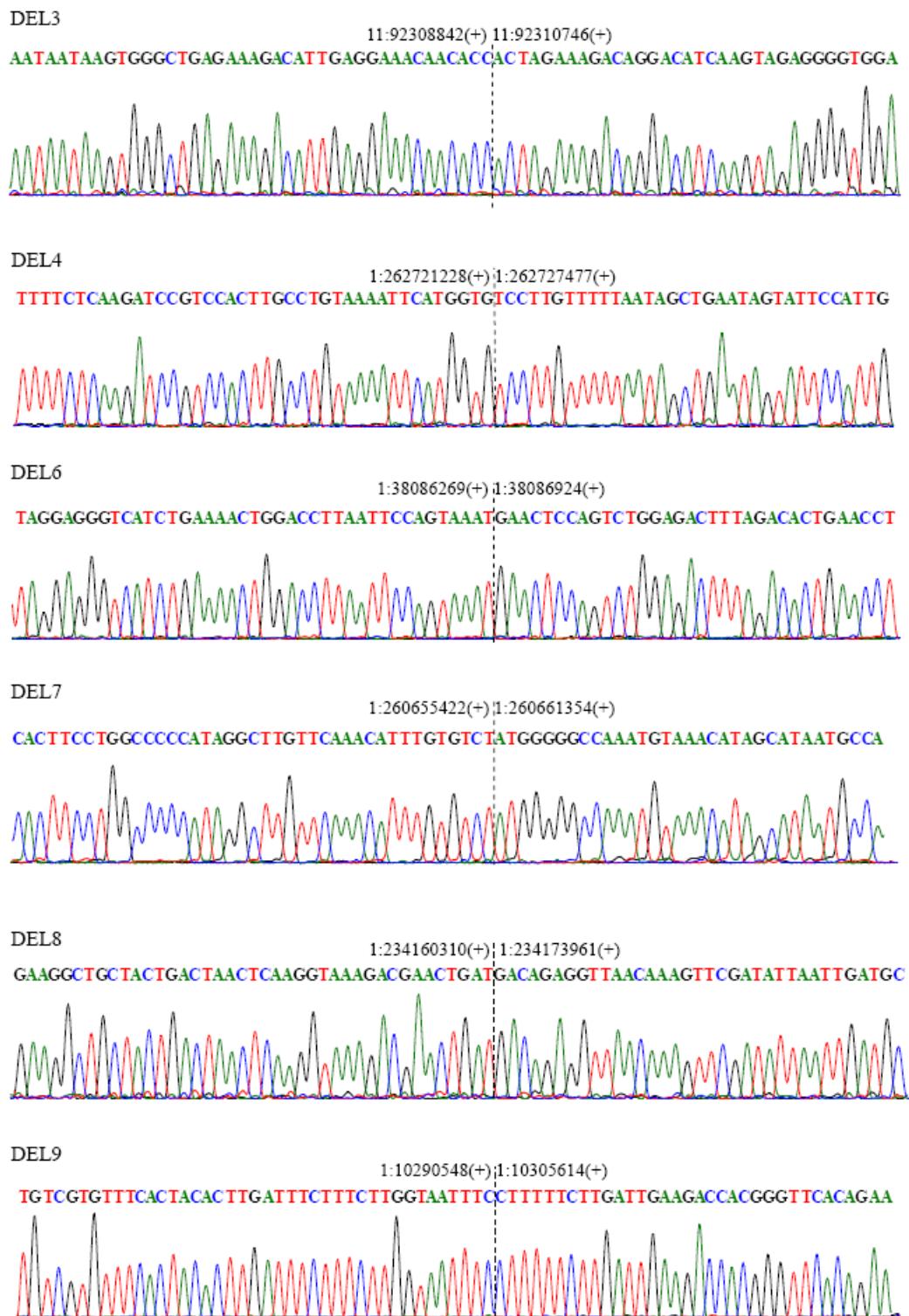


Figure B: Sanger sequencing of candidate deletion breakpoints.

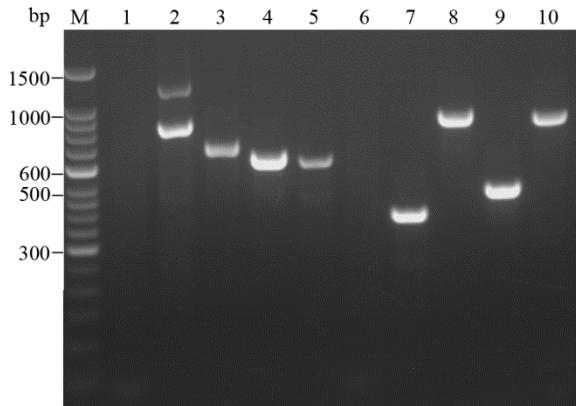


Figure C: PCR results of candidate inversion breakpoints. Lane M: Marker; Lane 1–10 represent inversion breakpoints of INV1–INV10, respectively. For large inversions such as INV3, INV4, INV5, INV7, and INV9, only single-end breakpoints were tested.

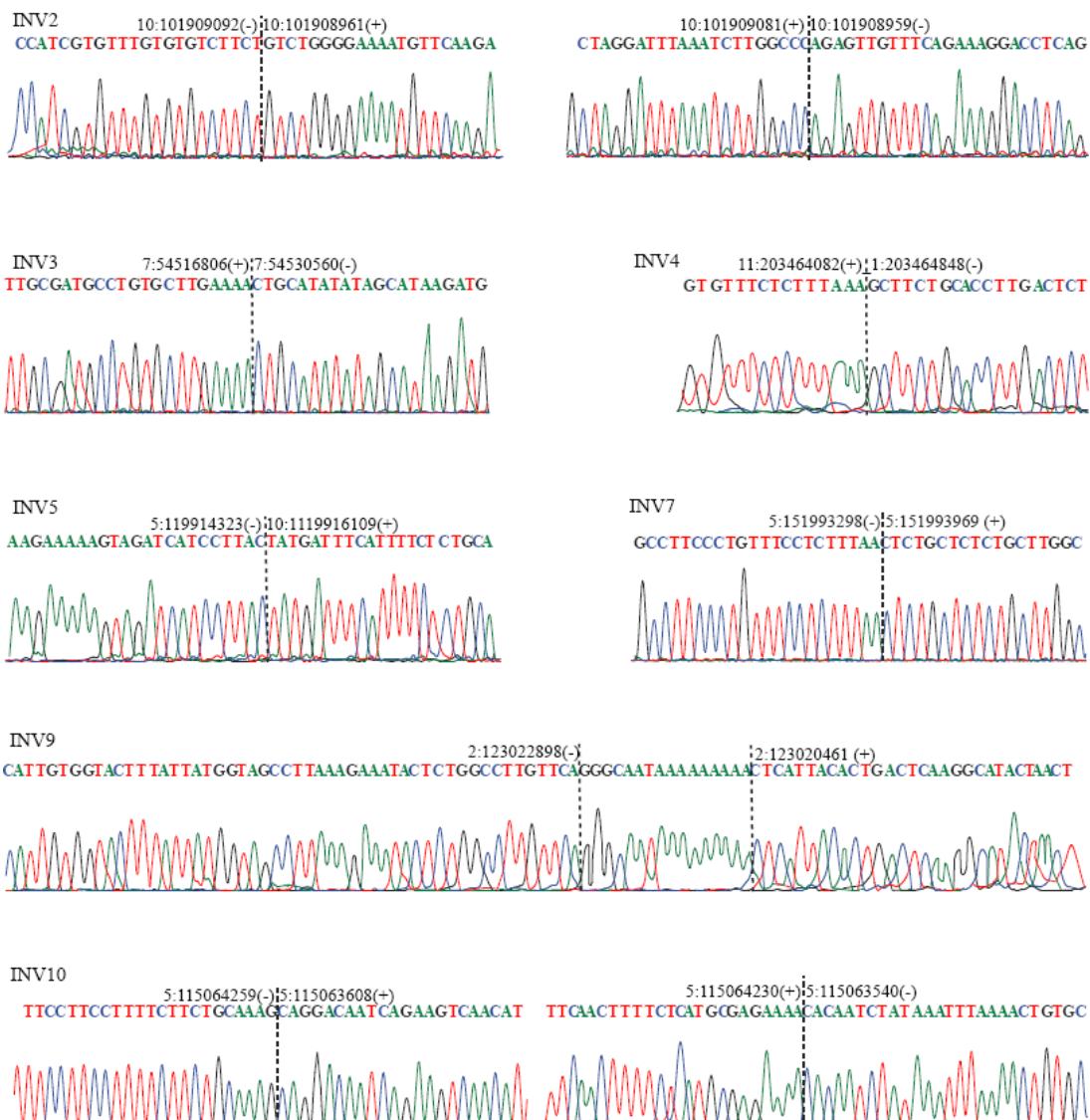


Figure D: Sanger sequencing of candidate inversion breakpoints.